

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 20, 2005, 19:25:58 ; Search time 165 Seconds
(without alignments)
1924.426 Million cell updates/sec

Title: ALLEN-724676-70493

Perfect score: 4338
Sequence: 1 MDVVDPDIFNRDPDRDHTL.....VETRPVDPFAPSNIYIQE 821

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|---------------------|
| 1 | 4288 | 98.8 | 847 | 8 | ADR39751 Human kin |
| 2 | 4196 | 96.7 | 833 | 6 | AAO30330 Human MAP |
| 3 | 4196 | 96.7 | 833 | 8 | ADM72219 Human TAS |
| 4 | 4196 | 96.7 | 833 | 8 | ADP24693 PRO polyp |
| 5 | 4057 | 93.5 | 772 | 4 | ABG01438 Novel hum |
| 6 | 2421 | 55.8 | 495 | 7 | ADB37566 Neural th |
| 7 | 2421 | 55.8 | 495 | 7 | ADJ59822 Human hea |
| 8 | 1930 | 44.5 | 842 | 2 | AAVS5956 Human STE |
| 9 | 1930 | 44.5 | 846 | 6 | AAO30335 Human MAP |
| 10 | 1930 | 44.5 | 846 | 6 | ADP23570 PRO polyp |
| 11 | 1917.5 | 44.2 | 873 | 6 | ABG74448 Rat Germ |
| 12 | 1904.5 | 43.9 | 873 | 4 | AAW78346 Human pro |
| 13 | 1898 | 43.8 | 894 | 2 | AAVS5935 Human KHS |
| 14 | 1898 | 43.8 | 894 | 6 | AAO30333 Human pro |
| 15 | 1898 | 43.8 | 894 | 6 | ADP24927 PRO polyp |
| 16 | 1896 | 43.7 | 894 | 4 | AAW78345 Human pro |
| 17 | 1896 | 43.7 | 930 | 4 | AAW79329 Human pro |
| 18 | 1896 | 43.7 | 930 | 4 | AAW79330 Human pro |
| 19 | 1877 | 42.3 | 884 | 6 | AAO30334 Human MAP |
| 20 | 1840.5 | 42.4 | 855 | 4 | ABG20230 Novel hum |
| 21 | 1697 | 39.1 | 820 | 6 | AAO30332 Human MAP |
| 22 | 1694 | 39.1 | 819 | 6 | AAO30331 Human MAP |
| 23 | 1694 | 39.1 | 819 | 8 | ADL12640 Human ste |
| 24 | 1518 | 35.0 | 1218 | 4 | ABB62736 Drosophila |
| 25 | 1444 | 33.3 | 698 | 8 | ADN61489 Human KPP |

| | | | | | |
|----|--------|------|------|---|---------------------|
| 26 | 1394.5 | 32.1 | 644 | 8 | ABM63565 Human dia |
| 27 | 717.5 | 16.5 | 979 | 4 | ABB66102 Drosophila |
| 28 | 675 | 15.6 | 1109 | 2 | AAVS5953 Nematode |
| 29 | 668.5 | 15.4 | 911 | 2 | AAVS5957 Mouse STE |
| 30 | 668.5 | 15.3 | 1286 | 8 | ADK71845 Human kin |
| 31 | 663.5 | 15.3 | 1295 | 5 | AAO18508 Human ins |
| 32 | 663.5 | 15.3 | 1295 | 7 | ADG36898 Human GCK |
| 33 | 663.5 | 15.3 | 1295 | 8 | ADG36898 Human GCK |
| 34 | 663.5 | 15.3 | 1303 | 4 | AAW79153 Human pro |
| 35 | 663.5 | 15.3 | 1303 | 5 | AAO18507 Human ins |
| 36 | 663.5 | 15.3 | 1303 | 7 | ADG36900 Human GCK |
| 37 | 661.5 | 15.2 | 1135 | 8 | ADR39750 Human kin |
| 38 | 661.5 | 15.2 | 1303 | 4 | AAE10612 Human nov |
| 39 | 660.5 | 15.2 | 1312 | 7 | ADB34150 Human mls |
| 40 | 651 | 15.0 | 449 | 6 | ABP96448 STK4/Met- |
| 41 | 651 | 15.0 | 462 | 8 | AD140883 Human kin |
| 42 | 651 | 15.0 | 462 | 8 | ADL70266 LBR1305 p |
| 43 | 651 | 15.0 | 467 | 8 | ADL70268 Human Mbc |
| 44 | 651 | 15.0 | 487 | 8 | ADR89878 Human Mbc |
| 45 | 650 | 15.0 | 426 | 2 | AAW31603 Human pro |

ALIGNMENTS

| | | |
|----------|---|---|
| RESULT 1 | ADR39751 | standard; protein; 847 AA. |
| ID | ADR39751 | |
| XX | ADR39751; | |
| XX | 18-NOV-2004 (first entry) | |
| DE | Human kinase and phosphatase KPP-24 protein SEQ ID NO:24. | |
| XX | human; kinase and phosphatase protein; KPP; enzyme; cytosolic; | |
| XX | antitumor; antileukemic; anticonvulsant; nootropic; neuroprotective; | |
| XX | cerebroprotective; anti-HIV; antiallergic; antiinflammatory; | |
| XX | thyromimetic; gene therapy; cell proliferative disorder; cancer; | |
| XX | atherosclerosis; neurological disorder; epilepsy; Huntington's disease; | |
| XX | stroke; immune disorder; inflammatory disorder; AIDS; allergy; | |
| XX | developmental disorder; Hypothyroidism; Cushing's syndrome; infection; | |
| XX | KPP-24. | |
| OS | Homo sapiens. | |
| XX | EN | WO2004074453-A2. |
| XX | PD | 02-SEP-2004. |
| XX | PF | 20-FEB-2004; 2004WO-US005092. |
| XX | PR | 20-FEB-2003; 2003US-0449059P. |
| XX | PR | 19-MAR-2003; 2003US-0456932P. |
| XX | PR | 28-MAR-2003; 2003US-0458844P. |
| XX | PR | 09-APR-2003; 2003US-0461678P. |
| XX | PR | 17-APR-2003; 2003US-0463937P. |
| XX | PA | (INCY-) INCYTE CORP. |
| XX | PI | Ramkumar J, Marquis JP, Swarnakar A, Chawla NK, Tran UK; |
| XX | PI | Becha SP, Lee SY, Hafalia AJA, Richardson TW, Khare R, Jiang X; |
| XX | PI | Jackson AA, Yang J, Gotvad AE; |
| XX | DR | N-PDB; ADR39797. |
| XX | DR | WPI; 2004-635568/61. |
| XX | PT | New human kinases and phosphatases (KPP) for diagnosing, treating and |
| XX | PT | preventing diseases or conditions associated with aberrant KPP expression |
| XX | PT | e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections. |
| XX | PS | Claim 1, SEQ ID NO 24; 29pp; English. |

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OM protein - protein search, using sw model

Run on: May 20, 2005, 19:29:34 ; Search time 46 Seconds
(without alignments)
1717.260 Million cell updates/sec

Title: ALLEN-724676-70493

Perfect score: 4338
Sequence: 1 MDVVDPIFRDPDRHYDL.....VETRPVDDPTAPSNLYIQE 821

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR_79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 1694 | 39.1 | 819 | 2 A53714 | protein kinase (EC |
| 2 | 1291 | 29.8 | 829 | 2 T29372 | hypothetical prote |
| 3 | 710.5 | 16.4 | 1102 | 2 J06316 | probable protein k |
| 4 | 693.5 | 16.0 | 836 | 2 B96716 | probable serine/ch |
| 5 | 645 | 14.9 | 426 | 2 S71886 | Ste20-like protein |
| 6 | 639 | 14.7 | 1075 | 2 T27623 | hypothetical prote |
| 7 | 638.5 | 14.7 | 653 | 2 T34356 | hypothetical prote |
| 8 | 633.5 | 14.6 | 1080 | 2 T27622 | hypothetical prote |
| 9 | 624.5 | 14.4 | 1233 | 2 T30969 | serine/threonine p |
| 10 | 604.5 | 13.9 | 960 | 2 C96572 | protein F12M16.4 |
| 11 | 580.5 | 13.4 | 471 | 2 T39232 | probable serine ch |
| 12 | 575 | 13.3 | 1233 | 2 T34157 | serine/threonine p |
| 13 | 574 | 13.2 | 1206 | 2 T34021 | hypothetical prote |
| 14 | 562 | 13.0 | 1228 | 2 T18887 | hypothetical prote |
| 15 | 556 | 12.8 | 1231 | 2 T18532 | serine/threonine p |
| 16 | 551 | 12.7 | 652 | 2 T39722 | serine/threonine p |
| 17 | 544.5 | 12.6 | 312 | 2 T38525 | serine/threonine p |
| 18 | 534.5 | 12.3 | 490 | 2 T47946 | protein kinase hom |
| 19 | 529.5 | 12.2 | 1001 | 2 T17365 | serine/threonine p |
| 20 | 515 | 11.9 | 982 | 2 T18576 | serine-threonine k |
| 21 | 512 | 11.8 | 544 | 2 S40482 | serine/threonine-s |
| 22 | 512 | 11.8 | 545 | 2 G01773 | p21-activated prot |
| 23 | 508 | 11.7 | 1080 | 2 S48944 | hypothetical prote |
| 24 | 505.5 | 11.7 | 544 | 2 T49376 | p21 activated kina |
| 25 | 504.5 | 11.6 | 525 | 2 S58682 | protein kinase, p2 |
| 26 | 500.5 | 11.5 | 544 | 2 A57587 | beta-p21-activated |
| 27 | 498.5 | 11.5 | 658 | 2 T39500 | serine/threonine-s |
| 28 | 478 | 11.0 | 939 | 2 S28394 | probable serine/ch |
| 29 | 473.5 | 10.9 | 658 | 2 S60170 | protein kinase Pak |

| | | | | | |
|----|-------|------|------|----------|--------------------|
| 30 | 473.5 | 10.9 | 1230 | 2 T18256 | probable serine/ch |
| 31 | 473.5 | 10.9 | 1230 | 2 T18259 | serine/threonine p |
| 32 | 468 | 10.8 | 608 | 2 G96575 | probable MEK kinas |
| 33 | 465.5 | 10.7 | 1062 | 2 S46367 | protein kinase CDC |
| 34 | 459 | 10.6 | 113 | 2 T38216 | protein-serine/ch |
| 35 | 457 | 10.5 | 622 | 2 T15467 | hypothetical prote |
| 36 | 456 | 10.5 | 589 | 2 T38086 | serine/threonine-p |
| 37 | 447.5 | 10.3 | 1014 | 2 T31109 | myosin III - Atlan |
| 38 | 444 | 10.2 | 1135 | 1 A29813 | 132K ninaC protein |
| 39 | 444 | 10.2 | 1501 | 1 B29813 | 174K ninaC protein |
| 40 | 443 | 10.2 | 378 | 2 A96662 | hypothetical prote |
| 41 | 442 | 10.2 | 378 | 2 T26684 | hypothetical prote |
| 42 | 442 | 10.2 | 553 | 2 T01479 | hypothetical prote |
| 43 | 440.5 | 10.2 | 655 | 2 S51884 | probable protein k |
| 44 | 439 | 10.1 | 842 | 2 S60402 | protein kinase CIA |
| 45 | 433.5 | 10.0 | 487 | 2 A71407 | probable Ste20-lik |

ALIGNMENTS

RESULT 1

A53714 protein kinase (EC 2.7.1.37) Bl44 - human

N:Alternate names: GC kinase

C:Species: Homo sapiens (man)

C>Date: 07-Jul-1995 #sequence_reviseion 07-Jul-1995 #text_change 09-Jul-2004

C:Accession: A53714

R:Katz, P., Whalen, G., Kehrl, J.H.

J. Biol. Chem. 269, 16802-16809, 1994

A:Title: Differential expression of a novel protein kinase in human B lymphocytes. Prefe

A:Reference number: A53714, MUID:94266900, PMID:7515885

A:Accession: A53714

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-819 <KAT>

A:Cross-references: UNIPROT:Q12851, GB:U07349, NID:G531819, PID:AAA20968.1, PID:G53182C

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C:Keywords: ATP; phosphotransferase

F:13-272/Domain: protein kinase homology <KIN>

F:21-29/Region: protein kinase ATP-binding motif

| Query Match | 39.1% | Score | 1694 | ID | 2 | Length | 819 |
|-----------------------|-------|--------------------|---|------------|-----|--------|-----|
| Best Local Similarity | 41.8% | Pred. No. | 1.1e-61 | | | | |
| Matches | 362 | Conservative | 142 | Mismatches | 250 | Indels | 112 |
| Gaps | 18 | | | | | | |
| QY | 7 | DINRDPDRHYDL | QRLGSGTGEVFRKADKSGDLVALKMKVKEPDDVSTQKELIIL | 66 | | | |
| DB | 5 | DVALQDPDRDFELLQ | RVGAGTGDVYKARDVTSELAVKIVKLDPPDDISSLQOEITIL | 64 | | | |
| QY | 67 | KTCGRHNIVAVHSGSYLM | QLKMTCMERCGSGSIQDIYQVNGSISELQISVVCREVLGLA | 126 | | | |
| DB | 65 | RECRHPVNAVYISYSLN | DLMTCMERCGSGSIQDIYHAGPSEKRIAYCERRLGLH | 124 | | | |
| QY | 127 | YLHSQKKIRHDIGKANIL | INDAGSEVLADFGISAQIGATLARRLSFGITPYMAAPRYAAV | 186 | | | |
| DB | 125 | HMSQKKIRHDIGKANIL | LLOGDVKLADRGVSGELTASVAKRSRFGITPYMAAPRYAAV | 184 | | | |
| QY | 187 | ALMGKINELCDWSLGTAL | IELAELQPLFVDPVRLVFLMTSGYQPPLEKCKKMSAA | 246 | | | |
| DB | 185 | ERKGGYNELCDVVALG | ITALELQPLFHLHPMALMMSKSSFPQPLKLRKTWTQN | 244 | | | |
| QY | 247 | FHNPIKVTLLTKSPKPK | PSATKMLSHQLVSPGLNRLGILLDLKKNPGKG-PSIGDIED | 305 | | | |
| DB | 245 | FHNPIKVTLLTKSPKPK | PSATKMLSHQLVSPGLNRLGILLDLKKNPGKG-PSIGDIED | 303 | | | |
| QY | 306 | EEBELLPAIPRRIRSTR | SSLSGTPDACCRRMEFRKLGMETRPANTARLOP---- | 361 | | | |
| DB | 304 | EYTDW---PDTHTSGG | CGAPARTSEIQFHYKVGARRKKTDP-----LNEPWEEE | 354 | | | |
| QY | 362 | -----RDLRSSPKQ | LSSESSDDYDDVDIPTPAADTP-----PLP | 398 | | | |
| DB | 355 | WTLGKEELSGSLQSG | VEALERSILTRISASBFQELDSP---DDTMGTIKRAPFLGFLP | 411 | | | |

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OM protein - protein search, using sw model

Run on: May 20, 2005, 19:38:56 ; Search time 142 Seconds
(without alignments)
1934.019 Million cell updates/sec

Title: ALLEN-724676-70493

Perfect score: 4338
Sequence: 1 MDVVDPDIFNRDPDRHYDL.....VETRPVDDPTAPSNLYIOE 821

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|---------------------------------------|
| 1 | 4303 | 99.2 | 836 | 15 | US-10-425-114-39187 Sequence 39187, A |
| 2 | 4196 | 96.7 | 833 | 14 | US-10-303-683-17 Sequence 17, Appl |
| 3 | 2421 | 55.8 | 495 | 14 | US-10-198-070-48 Sequence 48, Appl |
| 4 | 2421 | 55.8 | 495 | 16 | US-10-408-765A-1628 Sequence 1628, Ap |
| 5 | 1930 | 44.5 | 842 | 10 | US-09-291-417-91 Sequence 21, Appl |
| 6 | 1930 | 44.5 | 846 | 14 | US-10-303-683-22 Sequence 22, Appl |
| 7 | 1930 | 44.5 | 848 | 15 | US-10-425-114-39246 Sequence 39246, A |
| 8 | 1917.5 | 44.2 | 873 | 9 | US-09-843-245-3 Sequence 3, Appl1 |
| 9 | 1898 | 43.8 | 894 | 10 | US-09-291-417-18 Sequence 18, Appl |
| 10 | 1898 | 43.8 | 894 | 14 | US-10-303-683-21 Sequence 21, Appl |
| 11 | 1877 | 43.3 | 884 | 14 | US-10-303-683-19 Sequence 19, Appl |
| 12 | 1697 | 39.1 | 820 | 14 | US-10-303-683-18 Sequence 18, Appl |
| 13 | 1694 | 39.1 | 819 | 14 | US-10-303-683-18 Sequence 18, Appl |

| | | | | | | |
|----|-------|------|------|----|-------------------|-------------------|
| 14 | 1014 | 23.4 | 322 | 16 | US-10-664-421-78 | Sequence 78, Appl |
| 15 | 675 | 15.6 | 1109 | 10 | US-09-291-417-88 | Sequence 88, Appl |
| 16 | 668.5 | 15.4 | 911 | 10 | US-09-291-417-92 | Sequence 92, Appl |
| 17 | 663.5 | 15.3 | 1295 | 10 | US-09-789-390-30 | Sequence 30, Appl |
| 18 | 663.5 | 15.3 | 1295 | 10 | US-09-789-390-32 | Sequence 32, Appl |
| 19 | 663.5 | 15.3 | 1295 | 10 | US-09-789-390-34 | Sequence 34, Appl |
| 20 | 663.5 | 15.3 | 1295 | 10 | US-09-789-390-37 | Sequence 37, Appl |
| 21 | 663.5 | 15.3 | 1295 | 10 | US-09-789-390-39 | Sequence 39, Appl |
| 22 | 663.5 | 15.3 | 1303 | 10 | US-09-789-390-35 | Sequence 35, Appl |
| 23 | 663.5 | 15.3 | 1303 | 10 | US-09-789-390-38 | Sequence 38, Appl |
| 24 | 661.5 | 15.2 | 1303 | 10 | US-09-789-390-9 | Sequence 9, Appl |
| 25 | 660.5 | 15.2 | 1312 | 14 | US-10-029-115-2 | Sequence 2, Appl1 |
| 26 | 660.5 | 15.2 | 1312 | 17 | US-10-493-164-1 | Sequence 1, Appl1 |
| 27 | 650 | 15.0 | 1332 | 17 | US-10-498-698-9 | Sequence 9, Appl1 |
| 28 | 649 | 15.0 | 1332 | 10 | US-09-789-390-7 | Sequence 7, Appl1 |
| 29 | 648.5 | 14.9 | 1268 | 15 | US-09-789-390-13 | Sequence 13, Appl |
| 30 | 647 | 14.9 | 1268 | 15 | US-10-353-690-122 | Sequence 122, App |
| 31 | 647 | 14.9 | 1360 | 9 | US-09-871-916-2 | Sequence 2, Appl1 |
| 32 | 647 | 14.9 | 1360 | 14 | US-10-355-975-14 | Sequence 14, Appl |
| 33 | 646 | 14.9 | 1212 | 14 | US-10-247-671-157 | Sequence 157, App |
| 34 | 646 | 14.9 | 1212 | 15 | US-10-168-582-9 | Sequence 9, Appl1 |
| 35 | 645 | 14.9 | 426 | 9 | US-09-906-397-4 | Sequence 4, Appl1 |
| 36 | 645 | 14.9 | 426 | 9 | US-09-862-027-52 | Sequence 52, Appl |
| 37 | 645 | 14.9 | 426 | 17 | US-10-772-636-42 | Sequence 42, Appl |
| 38 | 645 | 14.9 | 426 | 17 | US-10-989-228-52 | Sequence 52, Appl |
| 39 | 643.5 | 14.8 | 1165 | 14 | US-10-021-660-126 | Sequence 126, App |
| 40 | 643.5 | 14.8 | 1165 | 15 | US-10-211-462-89 | Sequence 89, Appl |
| 41 | 643 | 14.8 | 426 | 9 | US-09-862-027-54 | Sequence 54, Appl |
| 42 | 643 | 14.8 | 426 | 10 | US-09-291-417-84 | Sequence 84, Appl |
| 43 | 643 | 14.8 | 426 | 17 | US-10-989-228-54 | Sequence 84, Appl |
| 44 | 642 | 14.8 | 487 | 9 | US-09-810-808-8 | Sequence 8, Appl1 |
| 45 | 640.5 | 14.8 | 1273 | 10 | US-09-789-390-11 | Sequence 11, Appl |

ALIGNMENTS

RESULT 1
US-10-425-114-39187
Sequence 39187, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (5313) B
CURRENT APPLICATION NUMBER: US/10/425, 114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 39187
LENGTH: 836
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LIB4676-011-A2_FUL_PEP
US-10-425-114-39187

Query Match 99.2%; Score 4303; DB 15; Length 836;
Best Local Similarity 99.4%; Pred. No. 1,4e+261;
Matches 816; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 MDVVDPDIFNRDPDRHYDLRGGTYGVKFAKRVSGDIALRVKMPDDVSTLQ 60
Db 16 MDVVDPDIFNRDPDRHYDLRGGTYGVKFAKRVSGDIALRVKMPDDVSTLQ 75
QY 61 KRLILIKTRHANIYVHGSYIMLQKMTCEPCGAGSLQDIYQVTSLSRLQISTVCR 120
Db 76 KRLILIKTRHANIYVHGSYIMLQKMTCEPCGAGSLQDIYQVTSLSRLQISTVCR 135

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OM protein - protein search, using sw model

Run on: May 20, 2005, 19:31:59 ; Search time 25 Seconds
(without alignments)
2451.475 Million cell updates/sec

Title: ALLEN-724676-70493

Perfect score: 4338
Sequence: 1 MDVVDPIENRDRDHYDL.....VETRPVDDPTAPNTXIQE 821

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 4196 | 96.7 | 847 | 4 | US-09-949-016-11002 |
| 2 | 1930 | 44.5 | 842 | 4 | US-09-688-188B-91 |
| 3 | 1930 | 44.5 | 842 | 4 | US-09-291-417D-91 |
| 4 | 1898 | 43.8 | 894 | 4 | US-09-688-188B-18 |
| 5 | 1898 | 43.8 | 894 | 4 | US-09-291-417D-18 |
| 6 | 1697 | 39.1 | 827 | 4 | US-09-949-016-7807 |
| 7 | 1694 | 39.1 | 819 | 4 | US-09-976-594-369 |
| 8 | 977.5 | 22.5 | 276 | 2 | US-08-852-743-7 |
| 9 | 977.5 | 22.5 | 276 | 3 | US-09-185-370-7 |
| 10 | 681 | 15.7 | 463 | 4 | US-09-270-767-43524 |
| 11 | 675 | 15.6 | 1109 | 4 | US-09-688-188B-88 |
| 12 | 675 | 15.6 | 1109 | 4 | US-09-291-417D-88 |
| 13 | 668.5 | 15.4 | 911 | 4 | US-09-688-188B-92 |
| 14 | 668.5 | 15.4 | 911 | 4 | US-09-291-417D-92 |
| 15 | 668.5 | 15.4 | 966 | 4 | US-09-688-188B-154 |
| 16 | 668.5 | 15.4 | 966 | 4 | US-09-291-417D-154 |
| 17 | 647 | 14.9 | 1269 | 4 | US-09-645-456A-15 |
| 18 | 647 | 14.9 | 1269 | 4 | US-09-425-324A-15 |
| 19 | 647 | 14.9 | 1269 | 4 | US-09-645-791-15 |
| 20 | 647 | 14.9 | 1277 | 4 | US-09-645-456A-12 |
| 21 | 647 | 14.9 | 1277 | 4 | US-09-425-324A-12 |
| 22 | 647 | 14.9 | 1277 | 4 | US-09-645-791-12 |
| 23 | 647 | 14.9 | 1298 | 4 | US-09-645-456A-14 |
| 24 | 647 | 14.9 | 1298 | 4 | US-09-425-324A-14 |
| 25 | 647 | 14.9 | 1298 | 4 | US-09-645-791-14 |
| 26 | 647 | 14.9 | 1306 | 4 | US-09-645-456A-10 |
| 27 | 647 | 14.9 | 1306 | 4 | US-09-425-324A-10 |

| | | | | | | |
|----|-----|------|------|---|-------------------|-------------------|
| 28 | 647 | 14.9 | 1306 | 4 | US-09-645-791-10 | Sequence 10, Appl |
| 29 | 647 | 14.9 | 1324 | 4 | US-09-645-456A-13 | Sequence 13, Appl |
| 30 | 647 | 14.9 | 1324 | 4 | US-09-425-324A-13 | Sequence 13, Appl |
| 31 | 647 | 14.9 | 1324 | 4 | US-09-645-791-13 | Sequence 9, Appl |
| 32 | 647 | 14.9 | 1332 | 4 | US-09-645-456A-9 | Sequence 9, Appl |
| 33 | 647 | 14.9 | 1332 | 4 | US-09-425-324A-9 | Sequence 9, Appl |
| 34 | 647 | 14.9 | 1332 | 4 | US-09-645-791-9 | Sequence 9, Appl |
| 35 | 647 | 14.9 | 1353 | 4 | US-09-645-456A-11 | Sequence 11, Appl |
| 36 | 647 | 14.9 | 1353 | 4 | US-09-425-324A-11 | Sequence 11, Appl |
| 37 | 647 | 14.9 | 1353 | 4 | US-09-645-791-11 | Sequence 11, Appl |
| 38 | 647 | 14.9 | 1360 | 3 | US-09-393-569-2 | Sequence 2, Appl |
| 39 | 647 | 14.9 | 1360 | 4 | US-09-579-664B-14 | Sequence 14, Appl |
| 40 | 647 | 14.9 | 1360 | 4 | US-09-645-456A-34 | Sequence 34, Appl |
| 41 | 647 | 14.9 | 1360 | 4 | US-09-425-324A-34 | Sequence 34, Appl |
| 42 | 647 | 14.9 | 1360 | 4 | US-09-645-791-34 | Sequence 34, Appl |
| 43 | 647 | 14.9 | 1360 | 4 | US-10-355-975A-14 | Sequence 14, Appl |
| 44 | 645 | 14.9 | 426 | 2 | US-08-852-743-2 | Sequence 2, Appl |
| 45 | 645 | 14.9 | 426 | 2 | US-09-211-930-4 | Sequence 4, Appl |

ALIGNMENTS

| | | | | | | | | | |
|---|-----|--|------------------------------------|----|--|--|--|--|--|
| RESULT 1 | | | | | | | | | |
| US-09-949-016-11002 | | | | | | | | | |
| ; Sequence 11002, Application US/09949016 | | | | | | | | | |
| ; Patent No. 6812339 | | | | | | | | | |
| ; GENERAL INFORMATION: | | | | | | | | | |
| ; APPLICANT: VENTER, J. Craig et al. | | | | | | | | | |
| ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED | | | | | | | | | |
| ; FILE REFERENCE: C1001307 | | | | | | | | | |
| ; CURRENT APPLICATION NUMBER: US/09/949, 016 | | | | | | | | | |
| ; PRIOR FILING DATE: 2000-04-14 | | | | | | | | | |
| ; PRIOR APPLICATION NUMBER: 60/241, 755 | | | | | | | | | |
| ; PRIOR FILING DATE: 2000-10-20 | | | | | | | | | |
| ; PRIOR APPLICATION NUMBER: 60/237, 768 | | | | | | | | | |
| ; PRIOR FILING DATE: 2000-10-03 | | | | | | | | | |
| ; PRIOR APPLICATION NUMBER: 60/231, 498 | | | | | | | | | |
| ; PRIOR FILING DATE: 2000-09-08 | | | | | | | | | |
| ; NUMBER OF SEQ. ID NOS: 207012 | | | | | | | | | |
| ; SOFTWARE: FASTSEQ for Windows Version 4.0 | | | | | | | | | |
| ; SEQ ID NO 11002 | | | | | | | | | |
| ; LENGTH: 847 | | | | | | | | | |
| ; TYPE: PRT | | | | | | | | | |
| ; ORGANISM: Human | | | | | | | | | |
| US-09-949-016-11002 | | | | | | | | | |
| Query Match 96.7%; Score 4196; DB 4; Length 847; | | | | | | | | | |
| Best Local Similarity 99.5%; Pred. No. 0; | | | | | | | | | |
| Matches 795; Conservative 0; Mismatches 4; Indels 0; Gaps 0; | | | | | | | | | |
| QY | 1 | MDVVDPIENRDRDHYDL | QRLGGTYGVFARQVSGDLVAKVKNKPPDDVSTLQ | 60 | | | | | |
| DB | 15 | MDVVDPIENRDRDHYDL | QRLGGTYGVFARQVSGDLVAKVKNKPPDDVSTLQ | 74 | | | | | |
| QY | 61 | KEILLIKTGHANIVAHGSYTLWLOKIMCECGASLDDIYOVGSLSELOISVCRE | 120 | | | | | | |
| DB | 75 | KEILLIKTGHANIVAHGSYTLWLOKIMCECGASLDDIYOVGSLSELOISVCRE | 134 | | | | | | |
| QY | 121 | VLOGLAIVHSQKIHNDIKANILINDAGEVRLADFGISAQIGATTARLSFICTPYMA | 180 | | | | | | |
| DB | 135 | VLOGLAIVHSQKIHNDIKANILINDAGEVRLADFGISAQIGATTARLSFICTPYMA | 194 | | | | | | |
| QY | 181 | PEVAALVAKGYNELCDIWSLGTITALELQPLPDVHPLRVLFMTKSGYOPPRILEK | 240 | | | | | | |
| DB | 195 | PEVAALVAKGYNELCDIWSLGTITALELQPLPDVHPLRVLFMTKSGYOPPRILEK | 254 | | | | | | |
| QY | 241 | GKSAAFHNHFKITLTKSPKRSATKMLSHOVVSGINRGILTLDDLKKNPGKPSI | 300 | | | | | | |
| DB | 255 | GKSAAFHNHFKITLTKSPKRSATKMLSHOVVSGINRGILTLDDLKKNPGKPSI | 314 | | | | | | |
| QY | 301 | GDIEDEPELPPAIPRIRISTRSSISGIPDADCCRRHMEFKLRGMEFRPPANTARLQ | 360 | | | | | | |

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OM protein - protein search, using sw model

Run on: May 20, 2005, 19:26:34 ; Search time 177 Seconds

(without alignments)
2375.237 Million cell updates/sec

Title: ALLEN-724676-70493

Perfect score: 4338
Sequence: 1 MDVDPDIPFNDRPDHYDL.....VETRPVDDPTAPSNLYIQE 821

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 4196 | 96.7 | 833 | 1 | MAK1_HUMAN |
| 2 | 3707 | 85.5 | 827 | 1 | MAK1_MOUSE |
| 3 | 1947 | 44.9 | 878 | 2 | OZU2 |
| 4 | 1930 | 44.5 | 846 | 1 | MAK5_HUMAN |
| 5 | 1905.5 | 43.9 | 847 | 1 | MAK5_MOUSE |
| 6 | 1905.5 | 43.9 | 862 | 1 | MAK3_RAT |
| 7 | 1898 | 43.8 | 894 | 1 | MAK3_HUMAN |
| 8 | 1882.5 | 43.4 | 823 | 2 | O68F04 |
| 9 | 1694 | 39.1 | 819 | 1 | MAK2_HUMAN |
| 10 | 1688 | 38.9 | 812 | 2 | O68V03 |
| 11 | 1652.5 | 38.5 | 821 | 1 | MAK2_MOUSE |
| 12 | 1652.5 | 38.1 | 881 | 1 | MAK3_MOUSE |
| 13 | 1633.5 | 37.7 | 947 | 2 | O6ML18 |
| 14 | 1632.5 | 37.6 | 947 | 2 | O6SYA1 |
| 15 | 1518 | 35.0 | 1218 | 2 | O3V8R6 |
| 16 | 1444 | 33.3 | 675 | 2 | O7Z266 |
| 17 | 1404.5 | 32.4 | 632 | 2 | O7Z299 |
| 18 | 1291 | 29.8 | 829 | 2 | OQ3290 |
| 19 | 1005.5 | 23.2 | 318 | 2 | O7QGN6 |
| 20 | 759 | 17.5 | 406 | 2 | O6PEQ2 |
| 21 | 747 | 17.2 | 1042 | 2 | O7KV89 |
| 22 | 721.5 | 16.6 | 737 | 2 | O661X1 |
| 23 | 721 | 16.6 | 1200 | 2 | O7KV90 |
| 24 | 721 | 16.6 | 1504 | 2 | O3W002 |
| 25 | 720 | 16.6 | 1102 | 2 | O7KV88 |
| 26 | 710.5 | 16.4 | 1102 | 2 | O7M3J7 |
| 27 | 710.5 | 16.4 | 1534 | 2 | O7PIC2 |
| 28 | 709 | 16.3 | 916 | 1 | TNIK_MOUSE |
| 29 | 704.5 | 16.2 | 855 | 2 | O8LK77 |
| 30 | 699.5 | 16.1 | 1120 | 2 | O9LOM1 |
| 31 | 699 | 16.1 | 829 | 2 | O871H9 |

| | | | | | |
|----|-------|------|------|---|------------|
| 32 | 699 | 16.1 | 842 | 2 | O9FN03 |
| 33 | 693.5 | 16.0 | 836 | 2 | O24527 |
| 34 | 690 | 15.9 | 461 | 2 | O61125 |
| 35 | 682 | 15.7 | 825 | 2 | O8SAR1 |
| 36 | 681.5 | 15.7 | 825 | 2 | O9ARL7 |
| 37 | 677.5 | 15.6 | 1082 | 2 | O8T8M3 |
| 38 | 672 | 15.5 | 1087 | 2 | O9XYC3 |
| 39 | 672 | 15.5 | 1096 | 2 | O95217 |
| 40 | 668.5 | 15.4 | 966 | 1 | STKA_MOUSE |
| 41 | 666.5 | 15.4 | 1072 | 2 | O814B5 |
| 42 | 661.5 | 15.2 | 1332 | 1 | MAK6_HUMAN |
| 43 | 660 | 15.2 | 809 | 2 | O6Y1C1 |
| 44 | 658 | 15.2 | 688 | 2 | O6Y2W8 |
| 45 | 654.5 | 15.1 | 420 | 2 | O7SYN3 |

ALIGNMENTS

REPORT 1
MAK1_HUMAN STANDARD, PRT: 833 AA.
AC Q92918; 10-OCT-2003 (Ref. 42, Created)
BT 10-OCT-2003 (Ref. 42, Last sequence update)
DT 10-OCT-2003 (Ref. 44, Last annotation update)
DE 85-JUN-2004 (Ref. 44, Last annotation update)
DE Mitogen-activated protein kinase kinase kinase 1 (EC 2.7.1.37)
DE (MAPK/ERK kinase kinase kinase 1) (MEKK 1)
DE (Hematopoietic progenitor kinase)
GN Name=MAPK1; Synonyms=HPK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND INTERACTION WITH
RP MAP3K1.
RC TISSUE=Fetal liver;
RX MEDLINE=96421968; PubMed=8824585;
R1 Hu M.C.-T., Qiu W.R., Wang X., Meyer C.F., Tan T.-H.,
R2 "Human HPK1, a novel human hematopoietic progenitor kinase that
R3 activates the JNK/SAPK kinase cascade.";
R4 Genes Dev. 10:2251-2264(1996).
CC -1- FUNCTION: May play a role in the response to environmental stress.
CC -1- Appears to act upstream of the JUN N-terminal pathway. May play a
CC -1- role in hematopoietic lineage decisions and growth regulation.
CC -1- Catalytic Activity: ATP + a protein = ADP + a phosphoprotein.
CC -1- COFACTOR: Magnesium.
CC -1- SUBUNIT: Interacts with MAP3K1.
CC -1- TISSUE SPECIFICITY: Expressed primarily in hematopoietic organs,
CC including bone marrow, spleen and thymus. Also expressed at very
CC low levels in lung, kidney, mammary glands and small intestine.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. STE20
CC subfamily.
CC -1- SIMILARITY: Contains 1 CNH domain.
CC
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CC
CC EMBL: U66464; AAB97983.1; -.
CC HSSP: Q13153; 1F3M.
CC Inact: Q92918; -.
CC Genew: HGNC:6863; MAP4K1.
CC MIM: 601983; -.
CC DR GO: GO:000524; F:ATP binding; IDA.
CC DR GO: GO:0004674; F:protein serine/threonine kinase activity; IDA.
CC DR GO: GO:0007257; P:activation of JNK; TAS.
CC DR GO: GO:0006468; P:protein amino acid phosphorylation; IDA.